RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 532,153
Source: PCT
Date Processed by STIC: 4-28-05

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 04/28/2005
PATENT APPLICATION: US/10/532,153   TIME: 16:26:58

Input Set : A:\Seq Listing.ST25.txt
Output Set: N:\CRF4\04272005\J532153.raw

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    3 <110> APPLICANT: Evolutionary Genomics LLC
    5 <120> TITLE OF INVENTION: Development of Therapeutics for the Treatment of
    6       Endotoxin-Mediated Diseases
    8 <130> FILE REFERENCE: GENO200.3.1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/532,153
C--> 10 <141> CURRENT FILING DATE: 2005-04-20
   10 <150> PRIOR APPLICATION NUMBER: 10/100,422
   11 <151> PRIOR FILING DATE: 2002-03-18
   13 <160> NUMBER OF SEQ ID NOS: 40
   15 <170> SOFTWARE: PatentIn version 3.2
   17 <210> SEQ ID NO: 1
   18 <211> LENGTH: 2427
   19 <212> TYPE: DNA
   20 <213> ORGANISM: Pan troglodytes
   22 <400> SEQUENCE: 1
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   27 tatagcttct tcagtttccc agaactgcag gtgctggatt tatccaggtg tgaaatccag    180
   29 acaattgaag atggggcata tcagagccta agccacctct ccaccttaat attgacagga    240
   31 aaccccatcc agagtttagc cctgggagcc ttttctggac tatcaagttt acagaagctg    300
   33 gtggctgtgg agacaaatct agcatctcta gagaacttcc ccattggaca tctcaaaact    360
   35 ttgaaagaac ttaatgtggc tcacaatctt atccaatctt tcaaattacc tgagtatttt    420
   37 tctaatctga ccaatctaga gcacttggac ctttccagca acaagattca aagtatttat    480
   39 tgcacagact tgcgggttct acatcaaatg cccctactca atctctcttt agacctgtcc    540
   41 ctgaaccota tgaactttat ccaaccaggt gcatttaaag aaattaggct tcataagctg    600
   43 actttgagaa ataattttga tagtttaaat gtaatgaaaa cttgtattca aggtctggct    660
   45 ggtttagaag tccatcgttt ggttctggga gaatttagaa atgaaggaaa cttggaaaag    720
   47 tttgacaaat ctgctctaga gggcctgtgc aatttgacca ttgaagaatt ccgattagca    780
   49 tacttagact actacctcga tgatattatt gacttatta attgtttgac aaatgtttct    840
   51 tcattttccc tggtgagtgt gactattaaa agcgtaaaag acttttctta taatttcgga    900
   53 tggcaacatt tagaattagt taactgtaaa tttggacagt ttcccacatt gaaactcaaa    960
   55 tctctcaaaa ggcttacttt cacttccaac aaaggtggga atgctttttc agaagttgat   1020
   57 ctaccaagcc ttgagtttct agatctcagt agaaatggct tgagtttcaa aggttgctgt   1080
   59 tctcaaagtg attttgggac aaccagccta agtatttag atctgagctt caatggtgtt   1140
   61 attaccatga gttcaaactt cttgggctta gaacaactag aacatctgga tttccagcat   1200
   63 tccaatttga aacaaatgag tgagttttca gtattcctat cactcagaaa cctcatttac   1260
   65 cttgacattt ctcatactca caccagagtt gctttcaatg gcatcttcaa tggcttgtcc   1320
   67 agtctcgaag tcttgaaaat ggctggcaat tctttccagg aaaacttcct tccagatatc   1380
   69 ttcacagagc tgagaaactt gaccttcctg gacctctctc agtgtcaact ggagcagttg   1440
   71 tctccaacag catttaactc actctccagt cttcaggtac taaatatgag ccacaacaac   1500
   73 ttctttttcat tggatacgtt tccttataag tgtctgaact ccctccaggt tcttgattac   1560
   75 agtctcaatc acataatgac ttccaaaaaa caggaactac agcattttcc aagtagtcta   1620
   77 gctttcttaa atcttactca gaatgacttt gcttgtactt gtgaacacca agtttcctg   1680
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RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/532,153**

DATE: 04/28/2005
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 79 caatggatca aggaccagag gcagctcttg gtggaagttg aacgaatgga atgtgcaaca    1740
 81 ccttcagata agcagggcat gcctgtgctg agtttgaata tcacctgtca gatgaataag    1800
 83 accatcattg gtgtgtcggt cctcagtgtg cttgtagtat ctgttgtagc agttctggtc    1860
 85 tataagttct attttcacct gatgcttctt gctggctgca taaagtatgg tagaggtgaa    1920
 87 aacatctatg atgcctttgt tatctactca agccaggatg aggactgggt aaggaatgag    1980
 89 ctagtaaaga atttagaaga aggggtgcct ccatttcagc tctgccttca ctacagagac    2040
 91 tttattcccg gtgtggccat tgctgccaac atcatccatg aaggtttcca taaaagccga    2100
 93 aaggtgattg ttgtggtgtc ccagcacttc atccagagcc gctggtgtat ctttgaatat    2160
 95 gagattgctc agacctggca gtttctgagc agtcgtgctg gtatcatctt cattgtcctg    2220
 97 cagaaggtgg agaagaccct gctcaggcgg caggtggagc tgtaccgcct tctcagcagg    2280
 99 aacacttacc tggagtggga ggacagtgtc ctggggcggc acatcttctg gagacgactc    2340
101 agaaaagccc tgctggatgg taaatcatgg aatccagaag gaacagtggg tacaggatgc    2400
103 aattggcagg aagcaacatc tatctga                                        2427
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 2427
108 <212> TYPE: DNA
109 <213> ORGANISM: Pan troglodytes
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113 <221> NAME/KEY: CDS
114 <222> LOCATION: (1)..(2427)
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119   1               5                  10                  15
121 atc ccc gac aac ctc ccc ttc tca acc aag aac ctg gac ctg agc ttt       96
122 Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
123               20                  25                  30
125 aat ccc ctg agg cat tta ggc agc tat agc ttc ttc agt ttc cca gaa      144
126 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
127           35                  40                  45
129 ctg cag gtg ctg gat tta tcc agg tgt gaa atc cag aca att gaa gat      192
130 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
131       50                  55                  60
133 ggg gca tat cag agc cta agc cac ctc tcc acc tta ata ttg aca gga      240
134 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
135 65                  70                  75                  80
137 aac ccc atc cag agt tta gcc ctg gga gcc ttt tct gga cta tca agt      288
138 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
139               85                  90                  95
141 tta cag aag ctg gtg gct gtg gag aca aat cta gca tct cta gag aac      336
142 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
143               100                 105                 110
145 ttc ccc att gga cat ctc aaa act ttg aaa gaa ctt aat gtg gct cac      384
146 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
147           115                 120                 125
149 aat ctt atc caa tct ttc aaa tta cct gag tat ttt tct aat ctg acc      432
150 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
151       130                 135                 140
153 aat cta gag cac ttg gac ctt tcc agc aac aag att caa agt att tat      480
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154 Asn Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr
155 145               150               155               160
157 tgc aca gac ttg cgg gtt cta cat caa atg ccc cta ctc aat ctc tct      528
158 Cys Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser
159               165               170               175
161 tta gac ctg tcc ctg aac cct atg aac ttt atc caa cca ggt gca ttt      576
162 Leu Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe
163               180               185               190
165 aaa gaa att agg ctt cat aag ctg act ttg aga aat aat ttt gat agt      624
166 Lys Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser
167               195               200               205
169 tta aat gta atg aaa act tgt att caa ggt ctg gct ggt tta gaa gtc      672
170 Leu Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val
171       210               215               220
173 cat cgt ttg gtt ctg gga gaa ttt aga aat gaa gga aac ttg gaa aag      720
174 His Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys
175 225               230               235               240
177 ttt gac aaa tct gct cta gag ggc ctg tgc aat ttg acc att gaa gaa      768
178 Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu
179               245               250               255
181 ttc cga tta gca tac tta gac tac tac ctc gat gat att att gac tta      816
182 Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu
183               260               265               270
185 ttt aat tgt ttg aca aat gtt tct tca ttt tcc ctg gtg agt gtg act      864
186 Phe Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr
187       275               280               285
189 att aaa agc gta aaa gac ttt tct tat aat ttc gga tgg caa cat tta      912
190 Ile Lys Ser Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu
191       290               295               300
193 gaa tta gtt aac tgt aaa ttt gga cag ttt ccc aca ttg aaa ctc aaa      960
194 Glu Leu Val Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys
195 305               310               315               320
197 tct ctc aaa agg ctt act ttc act tcc aac aaa ggt ggg aat gct ttt     1008
198 Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe
199               325               330               335
201 tca gaa gtt gat cta cca agc ctt gag ttt cta gat ctc agt aga aat     1056
202 Ser Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn
203               340               345               350
205 ggc ttg agt ttc aaa ggt tgc tgt tct caa agt gat ttt ggg aca acc     1104
206 Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr
207               355               360               365
209 agc cta aag tat tta gat ctg agc ttc aat ggt gtt att acc atg agt     1152
210 Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser
211       370               375               380
213 tca aac ttc ttg ggc tta gaa caa cta gaa cat ctg gat ttc cag cat     1200
214 Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His
215 385               390               395               400
217 tcc aat ttg aaa caa atg agt gag ttt tca gta ttc cta tca ctc aga     1248
218 Ser Asn Leu Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg
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219                    405                    410                    415
221 aac ctc att tac ctt gac att tct cat act cac acc aga gtt gct ttc    1296
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223              420                    425                    430
225 aat ggc atc ttc aat ggc ttg tcc agt ctc gaa gtc ttg aaa atg gct    1344
226 Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala
227              435                    440                    445
229 ggc aat tct ttc cag gaa aac ttc ctt cca gat atc ttc aca gag ctg    1392
230 Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu
231         450                    455                    460
233 aga aac ttg acc ttc ctg gac ctc tct cag tgt caa ctg gag cag ttg    1440
234 Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu
235 465                    470                    475                    480
237 tct cca aca gca ttt aac tca ctc tcc agt ctt cag gta cta aat atg    1488
238 Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met
239              485                    490                    495
241 agc cac aac aac ttc ttt tca ttg gat acg ttt cct tat aag tgt ctg    1536
242 Ser His Asn Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu
243              500                    505                    510
245 aac tcc ctc cag gtt ctt gat tac agt ctc aat cac ata atg act tcc    1584
246 Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser
247         515                    520                    525
249 aaa aaa cag gaa cta cag cat ttt cca agt agt cta gct ttc tta aat    1632
250 Lys Lys Gln Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn
251         530                    535                    540
253 ctt act cag aat gac ttt gct tgt act tgt gaa cac caa agt ttc ctg    1680
254 Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu
255 545                    550                    555                    560
257 caa tgg atc aag gac cag agg cag ctc ttg gtg gaa gtt gaa cga atg    1728
258 Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met
259              565                    570                    575
261 gaa tgt gca aca cct tca gat aag cag ggc atg cct gtg ctg agt ttg    1776
262 Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu
263         580                    585                    590
265 aat atc acc tgt cag atg aat aag acc atc att ggt gtg tcg gtc ctc    1824
266 Asn Ile Thr Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu
267         595                    600                    605
269 agt gtg ctt gta gta tct gtt gta gca gtt ctg gtc tat aag ttc tat    1872
270 Ser Val Leu Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr
271         610                    615                    620
273 ttt cac ctg atg ctt ctt gct ggc tgc ata aag tat ggt aga ggt gaa    1920
274 Phe His Leu Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu
275 625                    630                    635                    640
277 aac atc tat gat gcc ttt gtt atc tac tca agc cag gat gag gac tgg    1968
278 Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp
279              645                    650                    655
281 gta agg aat gag cta gta aag aat tta gaa gaa ggg gtg cct cca ttt    2016
282 Val Arg Asn Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe
283         660                    665                    670
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285 cag ctc tgc ctt cac tac aga gac ttt att ccc ggt gtg gcc att gct        2064
286 Gln Leu Cys Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala
287         675                     680             685
289 gcc aac atc atc cat gaa ggt ttc cat aaa agc cga aag gtg att gtt        2112
290 Ala Asn Ile Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val
291         690                     695             700
293 gtg gtg tcc cag cac ttc atc cag agc cgc tgg tgt atc ttt gaa tat        2160
294 Val Val Ser Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr
295 705                     710             715                 720
297 gag att gct cag acc tgg cag ttt ctg agc agt cgt gct ggt atc atc        2208
298 Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile
299                 725             730                 735
301 ttc att gtc ctg cag aag gtg gag aag acc ctg ctc agg cgg cag gtg        2256
302 Phe Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Arg Gln Val
303             740             745                 750
305 gag ctg tac cgc ctt ctc agc agg aac act tac ctg gag tgg gag gac        2304
306 Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp
307         755                     760             765
309 agt gtc ctg ggg cgg cac atc ttc tgg aga cga ctc aga aaa gcc ctg        2352
310 Ser Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu
311         770                     775             780
313 ctg gat ggt aaa tca tgg aat cca gaa gga aca gtg ggt aca gga tgc        2400
314 Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys
315 785                     790             795                 800
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319                 805
322 <210> SEQ ID NO: 3
323 <211> LENGTH: 808
324 <212> TYPE: PRT
325 <213> ORGANISM: Pan troglodytes
327 <400> SEQUENCE: 3
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333 Ile Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe
334             20                  25                  30
337 Asn Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu
338         35                  40                  45
341 Leu Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp
342     50                  55                  60
345 Gly Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly
346 65                  70                  75                  80
349 Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser
350             85                  90                  95
353 Leu Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn
354             100                 105                 110
357 Phe Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His
358         115                 120                 125
361 Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/532,153

DATE: 04/28/2005
TIME: 16:26:59

Input Set : **A:\Seq Listing.ST25.txt**
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<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:8; Xaa Pos. 198,683
Seq#:9; Xaa Pos. 198,683
Seq#:11; Xaa Pos. 635
Seq#:12; Xaa Pos. 635
Seq#:17; Xaa Pos. 14,462
Seq#:18; Xaa Pos. 14,462
Seq#:23; Xaa Pos. 758
Seq#:24; Xaa Pos. 758

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/532,153**

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Input Set : **A:\Seq Listing.ST25.txt**
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1198 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:8
L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:624
M:341 Repeated in SeqNo=8
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:192
M:341 Repeated in SeqNo=9
L:1830 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:11
L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1920
L:2042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:624
L:2665 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:17
L:2665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:48
M:341 Repeated in SeqNo=17
L:2886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:3885 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:23
L:3885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:2304
L:4101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:752
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